

AGCATCCTGA	GTAATGAGTG	GCCTGGGCGG	GAGCAGGCGA	GGTGCCCGGA	GCCGTGTGGA	60
CCAGGAGGAG	CGCTTTCCAG	AGGGCCTGTG	GACGGGGGTC	GCTATGAGAT	CCTGCCCCCA	120
AGAGCAGTAC	TGGGATCCTC	TGCTGGGTAC	CTGCATGTCC	TGCAAAACCA	TTTGCAACCA	180
TCAGAGCCAG	CGCACCTGTG	CAGCCTTCTG	CAGGTCACTC	AGCTGCCCGA	AGGAGCAACG	240
CAAGTTCTAT	GACCATCTCC	TGAGGGACTG	CATCAGCTGT	GCCTCCATCT	GTGGACAGCA	300
CCCTAAGCAA	TGTGCATACT	TCTGTAGAA	CAAGCTCAGG	AGCCCACTGA	ACCTTCCACC	360
AGAGCTCAGG	AGACAGCGGA	GTGGAGAAAT	TGAAACAAT	TCAGACAACT	CGGGAAGGTA	420
CCAAGGATTG	GAGCACAGAG	GCTCAGAAAG	AAGTCCAGCT	CTCCCGGGGC	TGAAGCTGAG	480
TGCAGATCAG	GTGGCCCTGG	TCTACAGCAC	GCTGGGGCTC	TGCTGTGTG	CCGTCTCTTG	540
CTGCTTCCTG	GTGGCGGTGG	CCTGCTTCCT	CAAGAAGAGG	GGGGATCCCT	GCTCTGCCA	600
GCCCCGCTCA	AGGCCCCGTC	AAAGTCCGGC	CAAGTCTTCC	CAGGATCAAG	CGATGGAAGC	660
CGCGAGCCCT	GTGAGCACAT	CCCCGAGGCC	AGTGAGAGCC	TGCAGCTTCT	GCTTCCCTGA	720
GTGCAGGGGG	CCCACGCGAG	AGAGCGCAGT	CAGCGCTGGG	ACCCCGGACC	CCACTTGTGC	780
TGGAAGGTGG	GGGTGCCACA	CCAGGACCAC	AGTCTGCAG	CCTTGCCCA	ACATCCCA	840
CAGTGGCCTT	GGCATTGTGT	GTGTCCCTGC	CCAGGAGGGG	GGCCAGGGTG	CATAAATGGG	900
GOTCAGGGAG	GGAAAGGAGG	AGGGAGAGAG	ATGGAGAGGA	GGGAGAGAG	AAAGAGAGGT	960
GGGGAGAGGG	GAGAGAGATA	TGAGGAGAGA	GAGACAGAGG	AGGCAGAAAG	GGAGAGAAAC	1020
AGAGGAGACA	GAGAGGGAGA	GAGAGACAGA	GGGAGAGAGA	GACAGAGGGG	AAGAGAGGCA	1080
GAGAGGGAAA	GAGGCAGAGA	AGGAAAGAGA	CAGGCAGAGA	AGGAGAGAGG	CAGAGAGGGA	1140
GAGAGGCAGA	GAGGGAGAGA	GGCAGAGAGA	CAGAGAGGGA	GAGAGGGACA	GAGAGAGATA	1200
GAGCAGGAGG	TGCGGGCACT	CTGAGTCCCA	GTTCCAGAGT	CAGCTGTAGG	TCGTCATCAC	1260
CTAACACAC	GTGCAATAAA	GTCTCTGTGC	CTGCTGCTCA	CAGCCCCCGA	GAGCCCCCTCC	1320
TCCTGGAGAA	TAAACCTTT	GGCAGCTGCC	CTTCTCTAAA	AAAAAAAAAA	AAAAAA	1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
 290

FIGURE 1B

AGCAAGTTCA	GCCTGGTTAA	GTCCAAGCTG	AATTCCGGTC	AAAGTTCAAG
TAGTGATATG	GATGACTCCA	CAGAAAAGGA	GCAGTCAACG	CTTACTTCTT
GCCTTAAGAA	AAGAGAAGAA	ATGAAACTGA	AGGAGTGTGT	TTCCATCCTC
CCACGGAAGG	AAAGCCCCTC	TGTCCGATCC	TCCAAGACG	GAAAGCTGCT
GGCTGCAACC	TTGCTGCTGG	CACTGCTGTC	TTGCTGCCTC	ACGGTGGTGT
CTTTCTACCA	GGTGGCCGCC	CTGCAAGGGG	ACCTGGCCAG	CCTCCGGGCA
GAGCTGCAGG	GCCACCACGC	GGAGAAGCTG	CCAGCAGGAG	CAGGAGCCCC
CAAGGCCGGC	CTGGAGGAAG	CTCCAGCTGT	CACCGCGGGA	CTGAAAATCT
TTGAACCACC	AGCTCCAGGA	GAAGGCAACT	CCAGTCAGAA	CAGCAGAAAT
AAGCGTGCCG	TTCAGGGTCC	AGAAGAAACA	GTCACTCAAG	ACTGCTTGCA
ACTGATTGCA	GACAGTGAAA	CACCAACTAT	ACAAAAAGGA	TCTTACACAT
TTGTTCATG	GCTTCTCAGC	TTTAAAAGGG	GAAGTGCCCT	AGAAGAAAAA
GAGAATAAAA	TATTGGTCAA	AGAACTGGT	TACTTTTTTA	TATATGGTCA
GGTTTTATAT	ACTGATAAGA	CCTACGCCAT	GGGACATCTA	ATTACAGAGGA
AGAAGGTCCA	TGTCTTTGGG	GATGAATTGA	GTCTGGTGAC	TTTGTTCGA
TGTATTCAAA	ATATGCCTGA	AACACTACCC	AATAATTCCCT	GCTATTACAG
TGGCATTGCA	AAACTGGAAG	AAGGAGATGA	ACTCCAACCT	GCAATACCAA
GAGAAAATGC	ACAAATATCA	CTGGATGGAG	ATGTCACATT	TTTTGGTGCA
TTGAAACTGC	TGTGACCTAC	TTACACCATG	TCTGTAGCTA	TTTTCTCCTC
TTTCTCTGTA	CCTCTAAGAA	GAAAGAATCT	AACTGAAAAAT	ACCAAAAAAA
AAAAAAAAAA	AAAAAGATCT	TTAATTAAGC	GGCCGCAAGC	TTATTCCCTT
TAGTAGG				

FIGURE 2A

MDDSTEREQS	RLTŞCLKKRE	EMKLKECVSI	LPRKESPSVR	SSKDGKLLAA
TLALLALLSCC	LTVVSFYQVA	ALQGDLASLR	AELQGHHA EK	LPAGAGAPKA
GLEEAPAVTA	GLKIFEPPAP	GEGNSSQNSR	NKRAVQGPEE	TVTQDCLQLI
ADSETPTIQK	GSYTFVPWLL	SFKRGŞALEE	KENKILVKET	GYFFIYGQVL
YTDKTYAMGH	LIQRKKVHVF	GDEİSLVTLE	RCIQNMPETİ	PNNSCYSAGI
AKLEEĞDELO	LAIPRENAQI	SLDGDVTFFG	ALKLL	

FIGURE 2B

MARRLWILSL	LAVTLTVALA	APSQKSKRRRT	SSDRMKQIED	KIEEILSKIY
HIENEIARIK	KLIGERTRSG	NSSQNSRNKR	AVQGPEETVT	QDCLQLIADS
ETPTIQKGSY	TFVPWLLSFK	RGSALEEKEN	KILVKETGYF	FIYGQVLYTD
KTYAMGHLIQ	RKKVHVFGDE	LSLVTLFRCI	QNMPETLPNN	SCYSAGIAKL
EEGDELQLAI	PRENAQISLD	GDVTFFGALK	LL	

(SEQ ID NO:3)

FIGURE 3

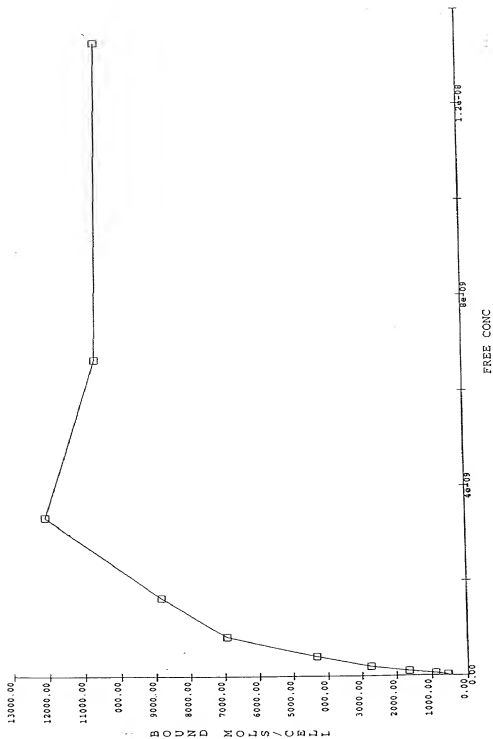


Figure 4A

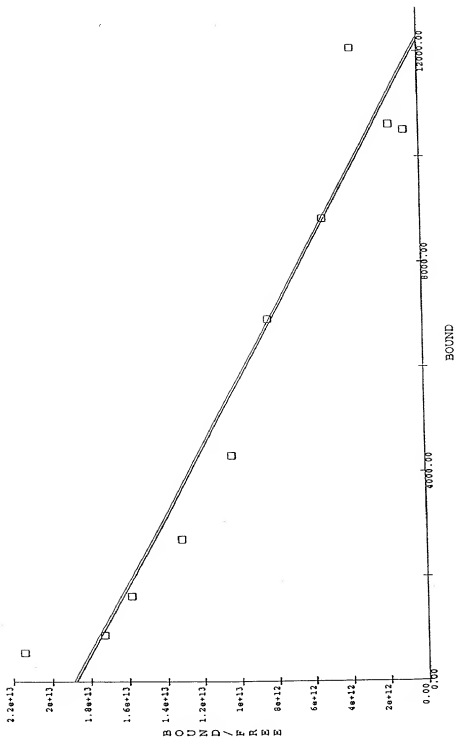


Figure 4B



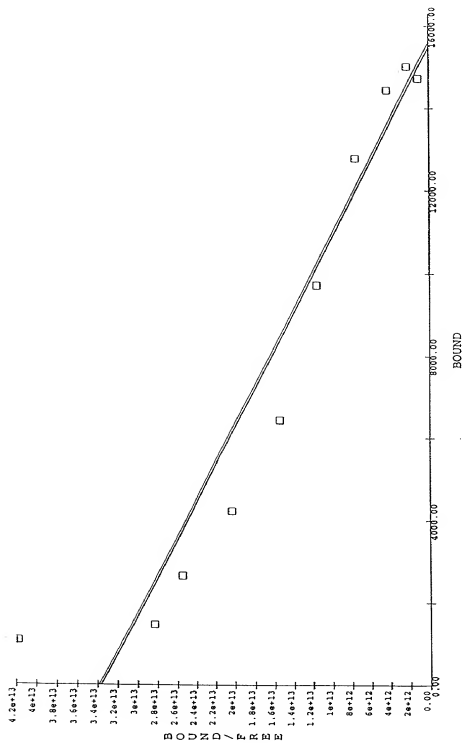


Figure 5B

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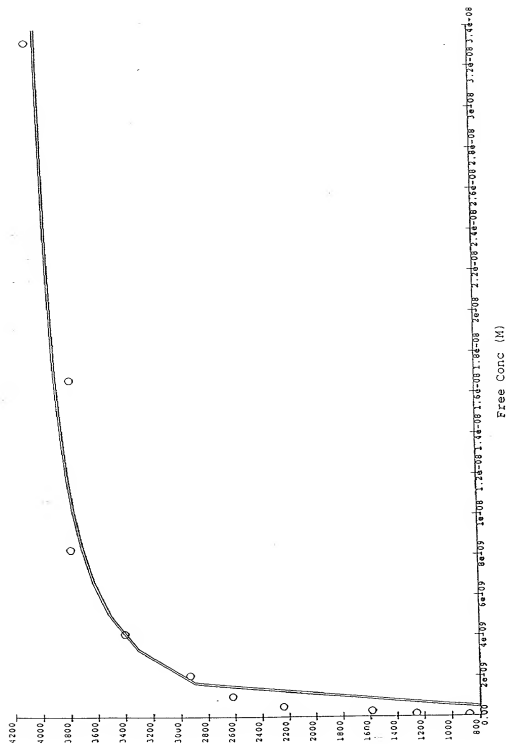


Figure 6A

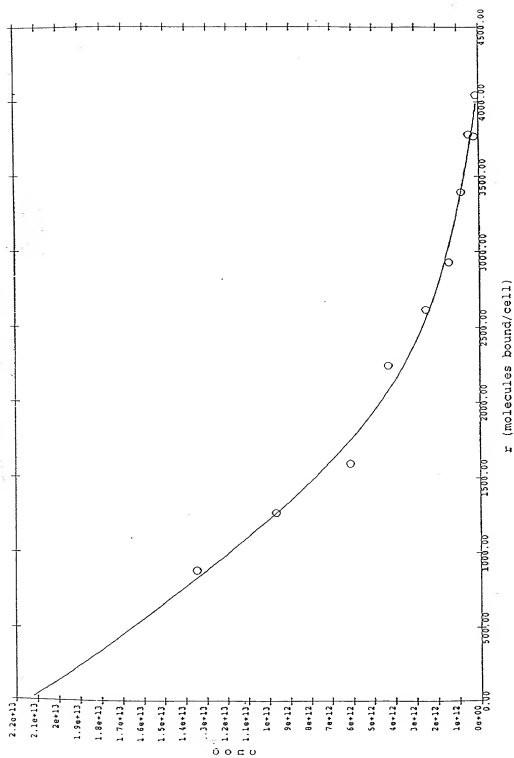


Figure 6B